What is claimed is:

1. A method for identifying a subject at risk of breast cancer, which comprises detecting the presence or absence of one or more polymorphic variations associated with breast cancer in a nucleic acid sample from a subject, wherein the one or more polymorphic variations are detected in a nucleotide sequence selected from the group consisting of:

(a) a nucleotide sequence in SEQ ID NO: 1-5;

(b) a nucleotide sequence which encodes a polypeptide encoded by a nucleotide sequence in SEQ ID NO: 1-5;

(c) a nucleotide sequence which encodes a polypeptide that is 90% or more identical to the amino acid sequence encoded by a nucleotide sequence in SEQ ID NO: 1-5;

(d) a fragment of a nucleotide sequence of (a), (b), or (c);

whereby the presence of the polymorphic variation is indicative of the subject being at risk of breast cancer.

2. The method of claim 1, which further comprises obtaining the nucleic acid sample from the subject.

3. The method of claim 1, wherein the one or more polymorphic variations are detected at one or more positions in SEQ ID NO: 1 selected from the group consisting of 139, 11799, 11851, 11851, 11963, 24282, 26849, 29633, 31254, 31967, 32920, 33929, 35599, 36101, 36101, 36340, 36405, 36517, 36777, 36992, 37645, 37868, 38440, 38440, 38532, 38532, 38547, 38547, 38712, 40684, 40860, 41213, 41419, 41613, 42407, 43440, 43440, 44247, 44247, 44247, 44247, 44677, 44677, 45256, 45256, 45536, 45536, 46153, 47546, 47697, 47944, 47944, 48530, 51102, 57090, 60093, 60439, 62694, 66260, 67295, 67295, 67304, 67731, 67731, 68555, 68555, 70429, 70875, 72360, 74228, 76802, 77664, 78803, 79263, 80810, 81020, 82426, 82783, 85912, 85912, 86135, 86135, 87877, 87877, 88043, 88043, 88206, 88343, 90701, 90701, 90974, 91060, 91087, 91594, 91594, 92302, 92384, 36517, and 44677.

4. The method of claim 1, wherein the one or more polymorphic variations are detected at one or more positions in SEQ ID NO: 1 selected from the group consisting of 11963, 36340, 36992, 37868, 41213, 41419, 41613, 42407, 44247, 44677, 45256, 45536, 51102, 72360, 36517, and 44677.

5. The method of claim 1, wherein the one or more polymorphic variations are detected at one or more positions in a region spanning positions 11851-24282, 36340-37868, 41213-41613, 70875-74228, 42407-45536, and 42407-51102 in SEQ ID NO: 1.

6. The method of claim 1, wherein the one or more polymorphic variations are detected at one or more positions in SEQ ID NO: 2 selected from the group consisting of 191, 1490, 3781, 3935, 4512, 7573, 8467, 9001, 9732, 13477, 13787, 13903, 14355, 15053, 15459, 17762, 19482, 19631, 22170, 22688, 22748, 23376, 23826, 23868, 24154, 25972, 26057, 26361, 26599, 26712, 26812, 27069, 32421, 33557, 35127, 35222, 35999, 36424, 37403, 39203, 39226, 41147, 46176, 50452, 52919, 60214, 61093, 62572, 63601, 65362, 65863, 66207, 66339, 69512, 70759, 71217, 73382, and 76307.

7. The method of claim 1, wherein the one or more polymorphic variations are detected at one or more positions in SEQ ID NO: 2 selected from the group consisting of 7573, 13903, 23826, 26057, 26361, 26599, 26812, 27069, 35127, 35222, 36424, 46176, 50452, 61093, 62572, and 70759.

8. The method of claim 1, wherein the one or more polymorphic variations are detected at one or more positions in a region spanning positions 23826-36424, 46176-62572, 4512-8467 or 13787-14355 in SEQ ID NO: 2.

9. The method of claim 1, wherein the one or more polymorphic variations are detected at one or more positions in SEQ ID NO: 3 selected from the group consisting of 107, 2157, 7300, 8233, 9647, 9868, 9889, 10621, 11003, 11507, 11527, 11718, 11808, 12024, 13963, 14300, 14361, 16287, 18635, 19365, 24953, 25435, 26847, 27492, 27620, 27678, 27714, 29719, 30234, 31909, 32153, 33572, 42164, 43925, 45031, 45655, 48350, 48418, 48563, 53189, 56468, 59358, 63761, 65931, 67040, 69491, 83308, 126545, 137592, and 147169.

10. The method of claim 1, wherein the one or more polymorphic variations are detected at one or more positions in SEQ ID NO: 3 selected from the group consisting of 107, 42164, 45031, 45655, 48563, 19365 and 14361.

11. The method of claim 1, wherein the one or more polymorphic variations are detected at one or more positions in a region spanning positions 42164-48563 in SEQ ID NO: 3.

12. The method of claim 1, wherein the one or more polymorphic variations are detected at one or more positions in SEQ ID NO: 4 selected from the group consisting of 174, 815, 3480, 9715, 14755, 15912, 19834, 19850, 20171, 20500, 20536, 23187, 25289, 25470, 28720, 29566, 30155, 30752, 32710, 32954, 33725, 33842, 36345, 38115, 39150, 40840, 41969, 42045, 43785, 44444, 44579, 45386, 46827, 47320, 47625, 47837, 47866, 49002, 49566, 52058, 52249, 52257, 52850, 53860, 54052, 54411,

55098, 55303, 59398, 59533, 60542, 61541, 62309, 72299, 73031, 73803, 80950, 82137, 96077, 96470, 98116, 98184, and 132952.

13. The method of claim 1, wherein the one or more polymorphic variations are detected at one or more positions in SEQ ID NO: 4 selected from the group consisting of 174, 815, 3480, 19834, 19850, 20171, 20500, 20536, 23187, 25470, 30155, 30752, 32710, 32954, 38115, 39150, 40840, 41969, 42045, 43785, 45386, 46827, 47320, 47625, 47837, 47866, 49002, 49566, 52058, 52257, 52850, 53860, 54052, 54411, 55303, 59398, 60542, 62309, 72299, 73031, 73803, and 98116.

14. The method of claim 1, wherein the one or more polymorphic variations are detected at one or more positions in a region spanning positions 174-32954, 38115-43785, 45386-52058, 52257-54411, 55303-73803 or 96470-98184 in SEQ ID NO: 4.

15. The method of claim 1, wherein the a polymorphic variation is detected at position 174 in SEQ ID NO: 5.

16. The method of claim 1, wherein two or more polymorphic variants are detected in two or more nucleotide sequences.

17. The method of claim 16, wherein polymorphic variants are detected at one or more positions selected from the group consisting of position 44247 in SEQ ID NO: 1, position 36424 in SEQ ID NO: 2, position 48563 in SEQ ID NO: 3, position 49002 in SEQ ID NO: 4 and position 174 in SEQ ID NO: 5.

18. The method of claim 1, wherein the one or more polymorphic variations are detected at one or more positions in linkage disequilibrium with one or more positions in claim 3, 6, 9, 12, or 15.

19. The method of claim 1, wherein detecting the presence or absence of the one or more polymorphic variations comprises:

hybridizing an oligonucleotide to the nucleic acid sample, wherein the oligonucleotide is complementary to a nucleotide sequence in the nucleic acid and hybridizes to a region adjacent to the polymorphic variation;

extending the oligonucleotide in the presence of one or more nucleotides, yielding extension products; and

detecting the presence or absence of a polymorphic variation in the extension products.

20. The method of claim 1, wherein the subject is a human.

21. A method for identifying a polymorphic variation associated with breast cancer proximal to an incident polymorphic variation associated with breast cancer, which comprises:

identifying a polymorphic variation proximal to the incident polymorphic variation associated with breast cancer, wherein the polymorphic variation is detected in a nucleotide sequence selected from the group consisting of:

(a) a nucleotide sequence in SEQ ID NO: 1-5;

(b) a nucleotide sequence which encodes a polypeptide encoded by a nucleotide sequence in SEQ ID NO: 1-5;

(c) a nucleotide sequence which encodes a polypeptide that is 90% or more identical to the amino acid sequence encoded by a nucleotide sequence in SEQ ID NO: 1-5;

(d) a fragment of a nucleotide sequence of (a), (b), or (c) comprising the polymorphic variation;

determining the presence or absence of an association of the proximal polymorphic variant with breast cancer.

22. The method of claim 21, wherein the incident polymorphic variation is at a position in claim 3, 6, 9, 12 or 15.

23. The method of claim 21, wherein the proximal polymorphic variation is within a region between about 5 kb 5' of the incident polymorphic variation and about 5 kb 3' of the incident polymorphic variation.

24. The method of claim 21, which further comprises determining whether the proximal polymorphic variation is in linkage disequilibrium with the incident polymorphic variation.

25. The method of claim 21, which further comprises identifying a second polymorphic variation proximal to the identified proximal polymorphic variation associated with breast cancer and determining if the second proximal polymorphic variation is associated with breast cancer.

26. The method of claim 25, wherein the second proximal polymorphic variant is within a region between about 5 kb 5' of the incident polymorphic variation and about 5 kb 3' of the proximal polymorphic variation associated with breast cancer.

27. An isolated nucleic acid comprising a nucleotide sequence selected from the group consisting of:

(a) a nucleotide sequence in SEQ ID NO: 1-5;

(b) a nucleotide sequence which encodes a polypeptide encoded by a nucleotide sequence in SEQ ID NO: 1-5;

(c) a nucleotide sequence which encodes a polypeptide that is 90% or more identical to the amino acid sequence encoded by a nucleotide sequence in SEQ ID NO: 1-5;

(d) a fragment of a nucleotide sequence of (a), (b), or (c); and

(e) a nucleotide sequence complementary to the nucleotide sequences of (a), (b), (c), or (d);

wherein the nucleotide sequence comprises one or more polymorphic variants associated with breast cancer selected from the group consisting of an adenine at position 11963 in SEQ ID NO: 1, a guanine at position 36340 in SEQ ID NO: 1, an adenine at position 36992 in SEQ ID NO: 1, a guanine at position 37868 in SEQ ID NO: 1, a cytosine at position 41213 in SEQ ID NO: 1, a guanine at position 41419 in SEQ ID NO: 1, a guanine at position 41613 in SEQ ID NO: 1, a cytosine at position 42407 in SEQ ID NO: 1, a cytosine at position 44247 in SEQ ID NO: 1, an adenine or cytosine at position 44677 in SEQ ID NO: 1, a thymine at position 45256 in SEQ ID NO: 1, a guanine at position 45536 in SEQ ID NO: 1, a cytosine at position 51102 in SEQ ID NO: 1, a guanine at position 72360 in SEQ ID NO: 1, a cytosine at position 36517 in SEQ ID NO: 1, a guanine at position 44677 in SEQ ID NO: 1, a guanine at position 7573 in SEQ ID NO: 2, a cytosine at position 13903 in SEQ ID NO: 2, an adenine at position 23826 in SEQ ID NO: 2, an adenine at position 26057 in SEQ ID NO: 2, a thymine at position 26361 in SEQ ID NO: 2, an adenine at position 26599 in SEQ ID NO: 2, an adenine at position 26812 in SEQ ID NO: 2, a cytosine at position 27069 in SEQ ID NO: 2, an adenine at position 35127 in SEQ ID NO: 2, a thymine at position 35222 in SEQ ID NO: 2, a cytosine at position 36424 in SEQ ID NO: 2, a cytosine at position 46176 in SEQ ID NO: 2, a cytosine at position 50452 in SEQ ID NO: 2, a guanine at position 61093 in SEQ ID NO: 2, an adenine at position 62572 in SEQ ID NO: 2, a guanine at position 70759 in SEQ ID NO: 2, an adenine at position 107 in SEQ ID NO: 3, a thymine at position 14361 in SEQ ID NO: 3, a guanine at position 19365 in SEQ ID NO: 3, a thymine at position 42164 in SEQ ID NO: 3, a cytosine at position 45031 in SEQ ID NO: 3, a thymine at position 45655 in SEQ ID NO: 3, a cytosine at position 48563 in SEQ ID NO: 3, a thymine at position 174 in SEQ ID NO: 4, an adenine at position 815 in SEQ ID NO: 4, a cytosine at position 3480 in SEQ ID NO: 4, a guanine at position 19834 in SEQ ID NO: 4, an adenine at position 19850 in SEQ ID NO: 4, a thymine at position 20171 in SEQ ID NO: 4, a thymine at position 20500 in SEQ ID NO: 4, a cytosine at position 20536 in SEQ ID NO: 4, a cytosine at position 23187 in SEQ ID NO: 4, a thymine at position 25470 in SEQ ID NO: 4, a thymine at position

30155 in SEQ ID NO: 4, a guanine at position 30752 in SEQ ID NO: 4, a thymine at position 32710 in SEQ ID NO: 4, a guanine at position 32954 in SEQ ID NO: 4, an adenine at position 38115 in SEQ ID NO: 4, a cytosine at position 39150 in SEQ ID NO: 4, a thymine at position 40840 in SEQ ID NO: 4, an adenine at position 41969 in SEQ ID NO: 4, a thymine at position 42045 in SEQ ID NO: 4, a guanine at position 43785 in SEQ ID NO: 4, a cytosine at position 45386 in SEQ ID NO: 4, an adenine at position 46827 in SEQ ID NO: 4, an adenine at position 47320 in SEQ ID NO: 4, a cytosine at position 47625 in SEQ ID NO: 4, a cytosine at position 47837 in SEQ ID NO: 4, an adenine at position 47866 in SEQ ID NO: 4, a cytosine at position 49002 in SEQ ID NO: 4, a thymine at position 49566 in SEQ ID NO: 4, a cytosine at position 52058 in SEQ ID NO: 4, a thymine at position 52257 in SEQ ID NO: 4, a thymine at position 52850 in SEQ ID NO: 4, a cytosine at position 53860 in SEQ ID NO: 4, a cytosine at position 54052 in SEQ ID NO: 4, a thymine at position 54411 in SEQ ID NO: 4, a cytosine at position 55303 in SEQ ID NO: 4, an adenine at position 59398 in SEQ ID NO: 4, an adenine at position 60542 in SEQ ID NO: 4, an adenine at position 62309 in SEQ ID NO: 4, a cytosine at position 72299 in SEQ ID NO: 4, a thymine at position 73031 in SEQ ID NO: 4, a guanine at position 73803 in SEQ ID NO: 4, and a thymine at position 98116, and an adenine at position 174 in SEQ ID NO: 5.

28. An oligonucleotide comprising a nucleotide sequence complementary to a portion of the nucleotide sequence of (a), (b), (c), or (d) in claim 27, wherein the 3' end of the oligonucleotide is adjacent to a polymorphic variation associated with breast cancer.

29. A microarray comprising an isolated nucleic acid of claim 27 linked to a solid support.

30. An isolated polypeptide encoded by the isolated nucleic acid sequence of claim 27.

31. A method for identifying a candidate molecule that modulates cell proliferation, which comprises:

(a) introducing a test molecule to a system which comprises a nucleic acid comprising a nucleotide sequence selected from the group consisting of:

(i) a nucleotide sequence in SEQ ID NO: 1-5;

(ii) a nucleotide sequence which encodes a polypeptide encoded by a nucleotide sequence in SEQ ID NO: 1-5;

(iii) a nucleotide sequence which encodes a polypeptide that is 90% or more identical to the amino acid sequence encoded by a nucleotide sequence in SEQ ID NO: 1-5;

(iv) a fragment of a nucleotide sequence of (i), (ii), or (iii); or

introducing a test molecule to a system which comprises a protein encoded by a nucleotide sequence of (i), (ii), (iii), or (iv); and

(b) determining the presence or absence of an interaction between the test molecule and the nucleic acid or protein,

whereby the presence of an interaction between the test molecule and the nucleic acid or protein identifies the test molecule as a candidate molecule that modulates cell proliferation.

32. The method of claim 31, wherein the system is an animal.

33. The method of claim 31, wherein the system is a cell.

34. The method of claim 31, wherein the nucleotide sequence comprises one or more polymorphic variations associated with breast cancer.

35. The method of claim 31, wherein the one or more polymorphic variations associated with breast cancer are at one or more positions in claim 3, 6, 9, 12 or 15.

36. A method for treating breast cancer in a subject, which comprises administering a candidate molecule identified by the method of claim 31 to a subject in need thereof, whereby the candidate molecule treats breast cancer in the subject.

37. A method for identifying a candidate therapeutic for treating breast cancer, which comprises:

(a) introducing a test molecule to a system which comprises a nucleic acid comprising a nucleotide sequence selected from the group consisting of:

(i) a nucleotide sequence in SEQ ID NO: 1-5;

(ii) a nucleotide sequence which encodes a polypeptide encoded by a nucleotide sequence in SEQ ID NO: 1-5;

(iii) a nucleotide sequence which encodes a polypeptide that is 90% or more identical to the amino acid sequence encoded by a nucleotide sequence in SEQ ID NO: 1-5;

(iv) a fragment of a nucleotide sequence of (i), (ii), or (iii); or

introducing a test molecule to a system which comprises a protein encoded by a nucleotide sequence of (i), (ii), (iii), or (iv); and

(b) determining the presence or absence of an interaction between the test molecule and the nucleic acid or protein,

whereby the presence of an interaction between the test molecule and the nucleic acid or protein identifies the test molecule as a candidate therapeutic for treating breast cancer.

38. The method of claim 37, wherein the test molecule inhibits cell proliferation or cell metastasis.

39. A method for treating breast cancer in a subject, which comprises contacting one or more cells of a subject in need thereof with a nucleic acid, wherein the nucleic acid comprises a nucleotide sequence selected from the group consisting of:

(a) a nucleotide sequence in SEQ ID NO: 1-5;

(b) a nucleotide sequence which encodes a polypeptide encoded by a nucleotide sequence in SEQ ID NO: 1-5;

(c) a nucleotide sequence which encodes a polypeptide that is 90% or more identical to the amino acid sequence encoded by a nucleotide sequence in SEQ ID NO: 1-5;

(d) a fragment of a nucleotide sequence of (a), (b), or (c); and

(e) a nucleotide sequence complementary to the nucleotide sequences of (a), (b), (c), or (d);

whereby contacting the one or more cells of the subject with the nucleic acid treats breast cancer in the subject.

40. The method of claim 39, wherein the nucleic acid is RNA or PNA.

41. The method of claim 40, wherein the nucleic acid is duplex RNA.

42. The method of claim 41, wherein a strand of the RNA comprises a nucleotide sequence selected from the group consisting of ACAACCGGAAGGUGUAUGA (SEQ ID NO: ); GCCAACCAAUGUGCUAUUC (SEQ ID NO: ); GAUCACCAUGGAGCCAAUU (SEQ ID NO: ); CUGUCACUCGAGAUCUUGA (SEQ ID NO: ); GAGUUGGAUAGCAAGACAA (SEQ ID NO: ) and CGUACGCGGAAUACUUCGA (SEQ ID NO: ).

43. A method for treating breast cancer in a subject, which comprises:

detecting the presence or absence of one or more polymorphic variations associated with breast cancer in a nucleic acid sample from a subject, wherein the one or more polymorphic variation are detected in a nucleotide sequence selected from the group consisting of:

(a) a nucleotide sequence in SEQ ID NO: 1-5;

(b) a nucleotide sequence which encodes a polypeptide encoded by a nucleotide sequence in SEQ ID NO: 1-5;

(c) a nucleotide sequence which encodes a polypeptide that is 90% or more identical to the amino acid sequence encoded by a nucleotide sequence in SEQ ID NO: 1-5;

(d) a fragment of a nucleotide sequence of (a), (b), or (c) comprising the polymorphic variation; and

administering a breast cancer treatment to a subject in need thereof based upon the presence or absence of the one or more polymorphic variations in the nucleic acid sample.

44. The method of claim 43, wherein the one or more polymorphic variations are detected at one or more positions in claim 3, 6, 9, 12 or 15.

45. The method of claim 43, wherein the breast cancer treatment comprises a nucleic acid comprising a nucleotide sequence complementary to a nucleotide sequence in SEQ ID NO: 1-5.

46. The method of claim 45, wherein the nucleic acid is a double stranded RNA.

47. The method of claim 46, wherein a strand of the RNA comprises a nucleotide sequence selected from the group consisting of ACAACCGGAAGGUGUAUGA (SEQ ID NO: ); GCCAACCAAUGUGCUAUUC (SEQ ID NO: ); GAUCACCAUGGAGCCAAUU (SEQ ID NO: ); CUGUCACUCGAGAUCUUGA (SEQ ID NO: ); GAGUUGGAUAGCAAGACAA (SEQ ID NO: ) and CGUACGCGGAAUACUUCGA (SEQ ID NO: ).

48. The method of claim 43, which further comprises extracting and analyzing a tissue biopsy sample from the subject.

49. The method of claim 43, wherein the treatment is chemotherapy, surgery, radiation therapy, and combinations of the foregoing.

50. The method of claim 49, wherein the chemotherapy is selected from the group consisting of cyclophosphamide (Cytoxan), methotrexate (Amethopterin, Mexate, Folex), fluorouracil (Fluorouracil, 5-Fu, Adrucil), cyclophosphamide, doxorubicin (Adriamycin), and combinations of the foregoing.

51. The method of claim 50, wherein the combinations are selected from the group consisting of cyclophosphamide (Cytoxan), methotrexate (Amethopterin, Mexate, Folex), and

fluorouracil (Fluorouracil, 5-Fu, Adrucil); cyclophosphamide, doxorubicin (Adriamycin), and fluorouracil; and doxorubicin and cyclophosphamide.

52. The method of claim 43, wherein the breast cancer treatment reduces breast cancer metastasis.

53. A method for detecting or preventing breast cancer in a subject, which comprises:

detecting the presence or absence of one or more polymorphic variations associated with breast cancer in a nucleic acid sample from a subject, wherein the polymorphic variation is detected in a nucleotide sequence selected from the group consisting of:

(a) a nucleotide sequence in SEQ ID NO: 1-5;

(b) a nucleotide sequence which encodes a polypeptide encoded by a nucleotide sequence in SEQ ID NO: 1-5;

(c) a nucleotide sequence which encodes a polypeptide that is 90% or more identical to the amino acid sequence encoded by a nucleotide sequence in SEQ ID NO: 1-5;

(d) a fragment of a nucleotide sequence of (a), (b), or (c) comprising the polymorphic variation; and

administering a breast cancer prevention procedure or detection procedure to a subject in need thereof based upon the presence or absence of the one or more polymorphic variations in the nucleic acid sample.

54. The method of claim 53, wherein the one or more polymorphic variations are detected at one or more positions in wherein the one or more polymorphic variations are detected at one or more positions in claim 3, 6, 9, 12 or 15.

55. The method of claim 53, wherein the breast cancer detection procedure is selected from the group consisting of a mammography, an early mammography program, a frequent mammography program, a biopsy procedure, a breast biopsy and biopsy from another tissue, a breast ultrasound and optionally ultrasound analysis of another tissue, breast magnetic resonance imaging (MRI) and optionally MRI analysis of another tissue, electrical impedance (T-scan) analysis of breast and optionally of another tissue, ductal lavage, nuclear medicine analysis (e.g., scintimammography), *BRCA1* and/or *BRCA2* sequence analysis results, thermal imaging of the breast and optionally of another tissue, and a combination of the foregoing.

56. The method of claim 53, wherein the breast cancer prevention procedure is selected from the group consisting of one or more selective hormone receptor modulators, one or more compositions that prevent production of hormones, one or more hormonal treatments, one or more biologic response modifiers, surgery, and drugs that delay or halt metastasis.

57. The method of claim 56, wherein the selective hormone receptor modulator is selected from the group consisting of tamoxifen, reloxifene, and toremifene; the composition that prevents production of hormones is an aramotase inhibitor selected from the group consisting of exemestane, letrozole, anastrozol, groserelin, and megestrol; the hormonal treatment is selected from the group consisting of goserelin acetate and fulvestrant; the biologic response modifier is an antibody that specifically binds herceptin/HER2; the surgery is selected from the group consisting of lumpectomy and mastectomy; and the drug that delays or halts metastasis is pamidronate disodium.

58. A method of targeting information for preventing or treating breast cancer to a subject in need thereof, which comprises:

detecting the presence or absence of one or more polymorphic variations associated with breast cancer in a nucleic acid sample from a subject, wherein the polymorphic variation is detected in a nucleotide sequence selected from the group consisting of:

(a) a nucleotide sequence in SEQ ID NO: 1-5;

(b) a nucleotide sequence which encodes a polypeptide encoded by a nucleotide sequence in SEQ ID NO: 1-5;

(c) a nucleotide sequence which encodes a polypeptide that is 90% or more identical to the amino acid sequence encoded by a nucleotide sequence in SEQ ID NO: 1-5;

(d) a fragment of a nucleotide sequence of (a), (b), or (c) comprising the polymorphic variation; and

directing information for preventing or treating breast cancer to a subject in need thereof based upon the presence or absence of the one or more polymorphic variations in the nucleic acid sample.

59. The method of claim 58, wherein the one or more polymorphic variations are detected at one or more positions in wherein the one or more polymorphic variations are detected at one or more positions in claim 3, 6, 9, 12 or 15.

60. The method of claim 58, wherein the information comprises a description of a breast cancer detection procedure, a chemotherapeutic treatment, a surgical treatment, a radiation treatment, a preventative treatment of breast cancer, and combinations of the foregoing.

61. A method of selecting a subject that will respond to a treatment of breast cancer, which comprises:

detecting the presence or absence of one or more polymorphic variations associated with breast cancer in a nucleic acid sample from a subject, wherein the polymorphic variation is detected in a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO: 1-5;

(b) a nucleotide sequence which encodes a polypeptide consisting of an amino acid sequence encoded by a nucleotide sequence in SEQ ID NO: 1-5 ;

(c) a nucleotide sequence which encodes a polypeptide that is 90% or more identical to an amino acid sequence encoded by a nucleotide sequence in SEQ ID NO: 1-5 ; and

(d) a fragment of a nucleotide sequence of (a), (b), or (c) comprising the polymorphic variation; and

selecting a subject that will respond to the breast cancer treatment based upon the presence or absence of the one or more polymorphic variations in the nucleic acid sample.

62. The method of claim 61, wherein the one or more polymorphic variations are detected at one or more positions in claim 3, 6, 9, 12 or 15.

63. A composition comprising a breast cancer cell and an antibody that specifically binds to a protein, polypeptide or peptide encoded by a nucleotide sequence identical to or 90% or more identical to a nucleotide sequence in SEQ ID NO: 1-12.

64. The composition of claim 63, wherein the antibody specifically binds to an epitope that comprises a leucine at amino acid position 359 in SEQ ID NO: 17, a leucine at amino acid position 378 in SEQ ID NO: 17, or an alanine at amino acid position 857 in SEQ ID NO: 17, or a ICAM5 polypeptide comprises a proline at amino acid position 352 or an alanine at amino acid position 348 in SEQ ID NO: 15.

65. A composition comprising a breast cancer cell and a RNA, DNA, PNA or ribozyme molecule comprising a nucleotide sequence identical to or 90% or more identical to a portion of a nucleotide sequence in SEQ ID NO: 1-12.

66. The composition of claim 63, wherein the RNA molecule is a short inhibitory RNA molecule.

67. A method for determining a risk of breast cancer in a subject, which comprises detecting the presence or absence of two or more polymorphic variations associated with breast cancer in a nucleic acid sample from a subject, wherein two or more of the polymorphic variations are detected in a nucleotide sequence selected from the group consisting of:

(a) a nucleotide sequence in SEQ ID NO: 1-5;

(b) a nucleotide sequence which encodes a polypeptide encoded by a nucleotide sequence in SEQ ID NO: 1-5;

(c) a nucleotide sequence which encodes a polypeptide that is 90% or more identical to the amino acid sequence encoded by a nucleotide sequence in SEQ ID NO: 1-5;

(d) a fragment of a nucleotide sequence of (a), (b), or (c);

whereby the presence of the polymorphic variation is indicative of the subject being at risk of breast cancer.

68. The method of claim 67, wherein two or more polymorphic variants are detected in two or more nucleotide sequences.

69. The method of claim 68, wherein the two or more polymorphic variations are at one or more positions in wherein the one or more polymorphic variations are detected at one or more positions in claim 3, 6, 9, 12 or 15.

70. The method of claim 69, wherein polymorphic variants are detected at one or more positions selected from the group consisting of position 44247 in SEQ ID NO: 1, position 36424 in SEQ ID NO: 2, position 48563 in SEQ ID NO: 3, position 49002 in SEQ ID NO: 4 and position 174 in SEQ ID NO: 5.